

# Dhirendra Kumar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4478207/publications.pdf>

Version: 2024-02-01

27  
papers

1,254  
citations

471509

17  
h-index

552781

26  
g-index

30  
all docs

30  
docs citations

30  
times ranked

2326  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating transcriptome and proteome profiling: Strategies and applications. <i>Proteomics</i> , 2016, 16, 2533-2544.	2.2	147
2	Proteogenomic Analysis of <i>Mycobacterium tuberculosis</i> By High Resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011445.	3.8	145
3	Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. <i>Cell Systems</i> , 2019, 8, 427-445.e10.	6.2	111
4	Transcriptome and venom proteome of the box jellyfish <i>Chironex fleckeri</i> . <i>BMC Genomics</i> , 2015, 16, 407.	2.8	103
5	A Systematic Analysis of Eluted Fraction of Plasma Post Immunoaffinity Depletion: Implications in Biomarker Discovery. <i>PLoS ONE</i> , 2011, 6, e24442.	2.5	87
6	Intragenic Enhancers Attenuate Host Gene Expression. <i>Molecular Cell</i> , 2017, 68, 104-117.e6.	9.7	85
7	Polyketide Quinones Are Alternate Intermediate Electron Carriers during Mycobacterial Respiration in Oxygen-Deficient Niches. <i>Molecular Cell</i> , 2015, 60, 637-650.	9.7	53
8	NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. <i>Nature Communications</i> , 2019, 10, 3072.	12.8	53
9	Decoding the function of bivalent chromatin in development and cancer. <i>Genome Research</i> , 2021, 31, 2170-2184.	5.5	48
10	GLIS3 is indispensable for TSH/TSHR-dependent thyroid hormone biosynthesis and follicular cell proliferation. <i>Journal of Clinical Investigation</i> , 2017, 127, 4326-4337.	8.2	47
11	MassWiz: A Novel Scoring Algorithm with Target-Decoy Based Analysis Pipeline for Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 2154-2160.	3.7	46
12	Expression profiling of lymph nodes in tuberculosis patients reveal inflammatory milieu at site of infection. <i>Scientific Reports</i> , 2015, 5, 15214.	3.3	43
13	Proteogenomic Analysis of <i>Bradyrhizobium japonicum</i> USDA110 Using Genosuite, an Automated Multi-algorithmic Pipeline. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3388-3397.	3.8	39
14	Integrated Transcriptomic-Proteomic Analysis Using a Proteogenomic Workflow Refines Rat Genome Annotation. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 329-339.	3.8	35
15	Choosing an Optimal Database for Protein Identification from Tandem Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 17-29.	0.9	25
16	Extensive Copy Number Variations in Admixed Indian Population of African Ancestry: Potential Involvement in Adaptation. <i>Genome Biology and Evolution</i> , 2014, 6, 3171-3181.	2.5	23
17	Integration Host Factor of <i>Mycobacterium tuberculosis</i> , mIHF, Compacts DNA by a Bending Mechanism. <i>PLoS ONE</i> , 2013, 8, e69985.	2.5	21
18	GLIS3 Transcriptionally Activates WNT Genes to Promote Differentiation of Human Embryonic Stem Cells into Posterior Neural Progenitors. <i>Stem Cells</i> , 2019, 37, 202-215.	3.2	21

#	ARTICLE	IF	CITATIONS
19	ProteoStatsâ€”a library for estimating false discovery rates in proteomics pipelines. <i>Bioinformatics</i> , 2013, 29, 2799-2800.	4.1	18
20	Spectrum of large copy number variations in 26 diverse Indian populations: potential involvement in phenotypic diversity. <i>Human Genetics</i> , 2012, 131, 131-143.	3.8	17
21	Discovery of rare proteinâ€”coding genes in model methylotroph <i>Methylobacterium extorquens</i> AM1. <i>Proteomics</i> , 2014, 14, 2790-2794.	2.2	17
22	Learning from Decoys to Improve the Sensitivity and Specificity of Proteomics Database Search Results. <i>PLoS ONE</i> , 2012, 7, e50651.	2.5	17
23	Proteogenomics of rare taxonomic phyla: A prospective treasure trove of protein coding genes. <i>Proteomics</i> , 2016, 16, 226-240.	2.2	12
24	False discovery rate: the Achillesâ€™ heel of proteogenomics. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	11
25	Proteogenomic Tools and Approaches to Explore Protein Coding Landscapes of Eukaryotic Genomes. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 1-10.	1.6	10
26	Gene-Rich Large Deletions Are Overrepresented in POAG Patients of Indian and Caucasian Origins. , 2014, 55, 3258.		9
27	Probing the Missing Human Proteome: A Computational Perspective. <i>Journal of Proteome Research</i> , 2015, 14, 4949-4958.	3.7	6